Supplemental Figure 2. Human-specific numts aligned with chimpanzee homologous nuclear site and human mtDNA.

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H:1:37.8  CAGATGGAAAGTCCTCCTTTATAGCTGACCTTATCCCCAT...CGTACGCCTAAGAATCCCTCCTGCTGCAAGATGGCCG
P:1:38.2  CAGATGGAAAGTCCTCCTTTATAGCTGACC----------...----------AGAATCCCTCCTGCTGCAAGATGGCCG
H:M:8835  ACTTCTTACCACAAGGCACACCTACACCCCTTATCCCCAT...CGTACGCCTAACCGCTAACATTACTGCAGGCCACCTA

H:1:213   CGATTTATTTATAGTTTTTCAAGGCATCACCCCGCTAAATCCCCTAGAAGTCCCACTCCTGGAGAAAGGGTCTATAGTTG
P:1:196   CGATTTATTTATAGTTTTTCAAG------------------------TACACTCTTTGGGGGAGAAAGGGTCTATAGTTG
H:M:9464  AGGAGGGCACTGGCCCCCAACAGGCATCACCCCGCTAAATCCCCTAGAAGTCCCACTCCTAAACACATCCGTATTACTCG

H:1:104   TACAGTATTGAAGCCTTATTTTAATCTAGTTTGATTAAACTAGATTGGTCTAGTTTGATTAAACTAGATTAAACTTCTTGGTCTAGGCACATGAATATTGTTGTGGGGAAGAGAATTCTGTATAATGTGATATGGATATT
P:1:105   TACAGTATTGAAGCCTTATTTTAATCTAGTTTGA------------------------------------------------------------------------------------CATTCTGTATAATATGATGTGGATACT
H:M:12.4  AAGTAGTCTAGTTTGAAGCTTAGGGAGAGCTGGGTTGTTTGGGTTGTGGCTCAGTGTCAGTTCGAGATAATAACTTCTTGGTCTAGGCACATGAATATTGTTGTGGGGAAGAGACTGATAATAAAGGTGGATGCGACAAT

H:2:33.8  CACGCCGTTGCTTCCAAGATGACTTGCTTGGTTAT...ATCTATTGCGCCATGTGAGGAGACGTTGCTGCTTTGCTCTGG
P:2a:34.5 CACGCCGTTGCTTCCAAGATGACTT----------...----------CCATGTGAGGAGACGTTGCTGCTTTGCTCTGG
H:M:1668  TAGGGGTTAGTCCTTGCTATATTATGCTTGGTTAT...ATCTATTGCGCCAGGTTTCAATTTCTATCGCCTATACTTTAT

H:2:49.3        TGGCCAGAACTTCCAACACTATGTTGTGTTGTTGTGTAGTGTAG...ACTTCATATTGCTTCCGTGGAGTGT...CACACAATAAACCCTAGGAAACCAATGAAGTTCTTAGCATGAAGGGCTGTTGAATT
P:2a_50.4       TGGCCAGAACTTCCAACACTATGTTG------------------...----------AATAGGAGCGGTGAG...ACGTTCCATCAATACCTAGCTCTTTGAGAGTTCTTAGCATGAAGGGCTGTTGAATT
H:M:6642        AGGACATAGTGGAAGTGAGCTACAACGTAGTACGTGTCGTGTAG...ATTTCATATTGCTTCCGTGGAGTGT...CACACGATAAACCCTAGGAAGCCAATTGATATCATAGCTCAGACCATACCTATGTA

H:2:81.7        TACAGATCTTAATAATAATTGTGTCTGTTTTTAGGC...ATTTGATAGTAAAGGAGGGGTCATATTAATAATAATAGGCTATAACCTGTTAAAAATAGTAGGTT
P:2a_83.5       TATGGATCTTAATAATAAT-----------------...-----------------------------------AGGCTATAACCTGTTAAAAATAGTAGGTT
H:M:7763        GGTTTAGACGTCCGGGAATTGCATCTGTTTTTAAGC...ATTTGATGGTAAGGGAGGGATCGTTGACCTCGTCTGTTATGTAAAGGATGCGTAGGGATGGGAGG

H:2:149   CCCTTTAGTCCTTACCTCTAAATCATCGTGGTGATT...GATGTGAGCCCGTCTAAACAGTTTCCCACCTGTGTCTACTT
P:2b:153  CCCTTTAGTCCTTACCTC------------------...------------------AGGTTTCCCACCTGTGTCTACTT
H:M:513   CGTGCTTGATGCTTGTCCCTTTTGATCGTGGTGATT...GATGTGAGCCCGTCTAAACATTTTCAGTGTATTGCTTTGAG

H:3:97.8        TCAGTAACATGTTAGTTGTATG------TAGTAACATAGTCTTGCTATGTTATGCC...TCCACCTTCGACCCTTAAATTTCATAAGCTCCCTCATGGGGAGCTAAATTTTTTT-AAGTATTTCATAATAATG
P:3:100         TCAGTAACATGTTAGTTGTATGAATGAATAG-----------------------...----------------------------TAAG-CACCTCATGGGGAGCTAATTTTTTTTTAAGAATTTCATAATAATG
H:M:1298        GTTTGCATTAATAAATTAAAGCTCCATAGGGTCTTCTCGTCTTGCTGTGTCATGCC...TCCACCTTCGACCCTTAAGTTTCATAAGGGCTATCGTAGTTTTCTGGGGTAGAAAATGTAGCCCATTTCTTGCC

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P:3:100         TCAGTAACATGTTAGTTGTATGAATGAATAG-----------------------...----------------------------TAAG-CACCTCATGGGGAGCTAATTTTTTTTTAAGAATTTCATAA
H:M:1298        GTTTGCATTAATAAATTAAAGCTCCATAGGGTCTTCTCGTCTTGCTGTGTCATGCC...TCCACCTTCGACCCTTAAGTTTCATAAGGGCTATCGTAGTTTTCTGGGGTAGAAAATGTAGCCCATTTC
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H:3:25.5       CACGTGGTGGATGGGTTCCCATCAGTAAGAGAAGACAATCACCATACAATCATAGCAAGCCAACGCCACTTATCCAGTGAACCAGCTCAAACAAACACTTCTCACCCTCTGCTTGTATCACATTTGCTAATAT
P:3:26.1       CACATGGTGGATGGGTTCCCATCAGTAAGAGAAGACAATCAC-----------------------------------------TATGCTCAAACACTTCTCACCCTCTGCTTGTATCACATTTGCTAATAT
H:M:10886      CTAACAACCCCCCTCCTAATACTAACTACCTGACTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCCAGCGAACCACTATCACGAAA-AAAACTCTACCTCTCTATACTAATCTCCCTACAAATC

***
P:3:26.1       CACATGGTGGATGGGTTCCCATCAGTAAGAGAAGAC-----------------------------------------AATCACTATGCTCAAACACTTCTCACCCTCTGCTTGTATCACATTTGCTAATAT
H:M:10886      CTAACAACCCCCCTCCTAATACTAACTACCTGACTCCTACCCCTCACAATCATGGCAAGCCAACGCCACTTATCCAGCGAACCACTATCACGAAA-AAAACTCTACCTCTCTATACTAATCTCCCTACAAATC
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H:3:68.8       AAAATGTTTGACCCGAGTTTGATATGGCTCTTGGGCTAGAGCCCAAGCATTGTTCGTTACATGGTCCATCATAGTCCTCTGGTAAATAGGTCTTTTACTTCTCACTCTCACCCCACAA
P:3_70.5       AAAATGTTTGACCCAAGTTTGATATGGCTCTTGGGCTAG----------------------------TTCTTAGTCCTCTGGTAAATAGGTCTTTTACTTCTCATTCTCACCCCACCA
H:M:12513      CCTAAGCTTCAAACTAGACTACTTCTCCATAATATTCATCCCTGTAGCATTGTTCGTTACATGGTCCATCATAGAATTCTCACTGTGATATATAAACTCAGACCCAAACATTAATCAG

H:4:79.1       TATTATCACAGCTTTGTTTCTCATTTTATCCTTTTTTTAACCTTTCC...GTATGTTTGGGATTTTTTAGACAATGGGCATTATCCTTGATTGCTCAGCTTGTAAGATGA-GGATGTTAATGCCT-CTATCC
P:4_52.4       TATTATCACAGCTTTGTTTCTCATTTTATC-----------------...------------------AG-CAATAGGTATTATCCTTGATTGCTCAGCTTGTAAGATGA-GGATGTTAATGCCT-CTATCC
H:M:2127       GGCGGGGTAAGGTTTGCCGAGTTCCTTTTACTTTTTTTAACCTTTCC...ATATGTTTGGGATTTTTTAGGTAGTGGGTGTTGAGCTTGAACGCTTT-CTTAATTGGTGGCTGCTTTTA-GGCCTACTATGG

H:4:55.9       CACTGGCATGATCATAACTCACCGCAGGAACTCCCCCCCAATAAAGCTAAAAC...GATTAGATACCGCACTATGGGCTCAAGCAATCCTCCCTTCTCAGGCTCCCAAGTAGCTAGGATTATAAGCAAGC
P:4_75.2       CACTGGCATGATCATAACTCACCGCAGGAACTCCC-----------------...------------------GGGCTCAAGCAATCCTCCCTTCTCAGGCTCCCAAGTAGCTAGGATTATAAGCAAGC
H:M:864        AAGCCGGCGTAAAGAGTGTTTTAGATCACCCCCTCCCCAATAAAGCTAAAAC...GATTAGATACCCCACTATGCTTAGCCCTAAACCTCAACAGTTAAATCAACAAAACTGCTCGCCAGAACACTACG

H:4:12.3       CAACCAAAACATCTTGACTCATGACCCCAGTGGTTTCGGTTATTTTCTATT...TCACTGGTACATGGTTAGTGTGTTGGTTAGTAGGCCTAGTGTGGAATCATTCCCAATGATGGAAGCAAGCTTTGTGGCA
P:4_12.5       CAACCACAACATCTTGACTCATGACCCCAA-------------------...--------------------TGTGT-GGAAGCACATGACCCCAATGTGTCATTCCCAGTG-TGGAAGCAAGCTTTGTGGCA
H:M:9239       AAAATTGTAATAAGCAGTGCTTGAATTATTTGGTTTCGGTTGTTTTCTATT...CCATTGGTATATGGTTAGTGTGTTGGTTAGTAGGCCTAGTATGAGGAGCGTTATGGAGTGGAAGTGAAATCACATGGCT

H:4:164        AAAATTTGCCCTTCTTTAATTGTCACCACCATCTGTTCAGTTTTTTT-GTTAGGGTTAATGA...TTAAAAGTTGAGAAAGCCATGTTGAATTCTAGAAATGCAAGATTTTTTCTTAATCATCTAAGCTATC
P:4_167        AAAACTTGCCCTTCTTTAATTGTCAAGACCACCTGTTCAGT---------------------...-------------------TGT-GAATTCTAGAAATGCAAGATTTTTTCTTAATCATCTAATCTATC
H:M:12151      GGTGGATGCGACAATGGATTTTACATAATGGGGGTATGAGTTTTTTTTGTTAGGGTTAACGA...TTAAAAGTTGAGAAAGCCATGTTGTTAGACATGGGGGCATGAGTTAGCAGTTCTTGTGAGCTTTCTC

H:4:47.5       CTACTTACTGTGACAATGCTTTAACACAGTGAGGGGTCAAGGTAGAGAAATGAGCCGT...ATTGGCGTGAAGGTAGCGGATTTCTTTGTAAATCAATTATTCACATTCCATAGAATTAAGTGAGACTTAACA
P:4_84.9       CTACTTACTGTGACAATGCTTTAACACAGTGAGGGGTCAA---------------------------------------TATTTCTTTGTAAATCAATTATTCACATTCCATAGAATTAAGTGAGATTTAACA
H:M:14882      GTTGCAAGCAGGAGGATAATGCCGATGTTTCAGGTTTCTGAGTAGAGAAATGATCCGT...ATTGGCGTGAAGGTAGCGGATGATTCAGCCATAATTTACGTCTCGAGTGATGTGGGCGATTGATGAAAAGGC

H:5:134        AGGAGCATGGTTAGGGAAGGCCTAACCATGGTGAGAAT...GCTATAATGAATAGTGATAGTATTATTCCTTCTAGGCATAGT...TGTAGGGCTCATGGCAAGGGTAAAAGGAGTGAAGGGTATTAAGAATG
P:5_137        AGGAGCATGGTTAGGGAAGGCCT-----TGGT----------...---------------AAGGCCTTCCCTATAAGCTGATA...GAGTGGTAATGGATGATAAGGAAGAACAGTGAAGGGTATTAAGAATG
H:M:10170      TATAATTGTCTGGGTCGCCTAGGAGGTCTGGTGAGAAT...GCTATAATGAACAGCGATAGTATTATTCCTTCTAGGCATAGT...TGTAGGGCTCATGGTAGGGGTAAAAGGAGGGCAATTTCTAGATCAAA
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H:5:73.1       CAAGATATAACAGAAAATAAGTGTATATTCAAGTCTTGAATATACATGACTCTCCAAAAAACACATAATTTGAATCAACACAACATTTAGGTTGGAAATGTCGTTCCTTTGTGTGTGAGTGTGTTCAGAAATA
P:5_42.2       CAAGATATAACAGAAAATAAGTGTATATTCAAG-------------------------------------------------AATTTAGGTTGGAAATGTCGTTCCTTTGTGTGTGAGTGTGTTCAGAAATA
H:M:10703      AATGCTAAAACTAATCGTCCCAACAATTATATTACTACCACTGACATGACTTTCCAAAAAGCACATAATTTGAATCAACACAACCACCCACAGCCTAATTATTAGCATCATCCCCCTACTATTTTTTAACCAA

H:5:166        ACTGATGTCACATAGACAGTTGGCATTTGTTTATGGATGAAAACCCTCTGTTGTCAGATTCACAATCTGATGTTTTGGTTAAACATGAATTTTAGGAAGCTCAGGATGGTATAAAATATGTGTGTATGCATG
P:5_169        ACTGATGTCACATAGACAGTTGGCATTTGTTTATGGATGAAAACC----------------------------------AAAACGTGAATTTTAGGAAGCTCAGGATGGTATAAAATATGTGTGTATGCATG
H:M:12048      TTAGCAGTTCTTGTGAGCTTTCTCGGTAAATAAGGGGTCGTAAGCCTCTGTTGTCAGATTCACAATCTGATGTTTTGGTTAAACTATATTTACAAGAGGAAAACCCGGTAATGATGTCGGGGTTGAGGGATA

H:7:145        TCAAATTATACAAAGTGCAAGGAGAAAAATAAAATAATAAAGGAGGTTAACATAAAGCACCCAAC...CACTCCACCTTACTACCAAACAGAGTGTGAGAATGAAAGAAATGCAACTTTCAATCACTAAGA
P:7_147        TCAAATTATACAAAGTGCAAGGAGAAAAA----ATAATAAAGGAGGTTA----------------...--------------------GGGAGTGTGAGAATGAAAGAAATGCAACTTTCAATCACTAAGA
H:M:1515       ATGGTAAGTGTACTGGAAAGTGCACTTGGACGAACCAGAGTGTAGCTTAACACAAAGCACCCAAC...CACTCCACCTTACTACCAGACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGCGATA

H:7:67.8       ACCTTGATATCTAACCTGCAGAGTCACTAATGTTTTCCAGTATGAAAACATTTCCAGC...CATAGAAGGCCCCACCCCTGTCTGTGCACAGATGAATATGAATCAAGAATGGTGCCCAGTGGGCAATGAAAAT
P:7_68.5       ACCTTGATATCTAACCTGCAGAGTCACTAATGTTTTCCAGTATGA-------------...--------------------GGTGTGCACAGATGAATATGAATCAAGAATGGTGCCCAGTGGGCAATGAAAAT
H:M:12862      CCTACACTCCAACTCATGAGACCCACAACAAATAGCCCTTCTAAACGCTAATCCAAGC...CATAGAAGGCCCCACCCCAGTCTCAGCCCTACTCCACTCAAGCACTATAGTTGTAGCAGGAATCTTCTTACTC

H:8:100.6      ATTTTATTCTTAGCTTATTAATATTCAGTATTTTCTTTAAAATTGATTGATGAAAAGGCG...GAGGATCAGGCAGGCAAACCTAAGTTATTAAGACATAGTCCTTTATCATTTGAGGAATTTATAATATT
P:8_98.4       ATTTTATTCTTAGCTTATTAATATTCAGTATTTTCTTTA----------------------...---------------AAACCTAAGTTATTAAGACATAGTCCTTTATCATTTGAGGAATTTATAATATT
H:M:14762      TAGCGGATGATTCAGCCATAATTTACGTCTCGAGTGATGTGGGCGATTGATGAAAAGGCG...GAGGATCAGGCAGGCGCCAAGGAGTGAGCCGAAGTTTCATCATGCGGAGATGTTGGATGGGGTGGGGA

H:11:72.9      ACTAGCCCGTTCATGAGGTAAGCCAAAAGGGGGTACATCCTACCAGGATTCGGAATA...GGAATGGACGTAGACAGATAATGCCTAATGTAATCAGAAACAAGCTGCTGAATTCAATGGAAGCTGCT
P:11_71.8      ACTAGCCCGTTCATGAGGTAAGCCAAAAGGGGGT------------------------...-------------ACAGATAATGCCTAATGTAATCAGAAACAAGCTGCTGAATTCAATGGAAGCTGCT
H:M:6543       TTCTGATTTTTCGGTCACCCTGAAGTTTATATTCTTATCCTACCAGGCTTCGGAATA...GGAATAGACGTAGACACACGAGCATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGT

H:11:122       TGATTTCCTTCCATCTGTGATAACTTCGTTGTTCTGAAATACAACGATGGTTTTT...GAGAATAATGATGTATGCTTTCCCTGGAAATCAGCTAGATCCAGAGTTCCCAAATGGTGGTCTATGGACC
P:11_122       TGATTTCCTTCCATCTGTGATAACTTCGTTGTTCTG-------------------...--------------------TCCCTGGAAATCAGCTAGATC-AGAGTTCCCAAATGCTGGTCTATGGACC
H:M:14561      TTTTGCGTATTGGGGTCATTGGTGTTCTTGTAGTTGAAATACAACGATGGTTTTT...GAGAATAATGATGTATGCTTTGTTTCTGTTGAGTGTGGGTTTAGTAATGGGGTTTGTGGGGTTTTCTTCT

H:12:40.0      GTTAAGGATGCATTTATTCAGATTTCATTTGTTTGGGTGCTAGTTTGGAGATAAATC...TTGTGATAAGGGTGGAGATGCATTTGCTCAGGATGCATTTGTTTGGCAGGTCCCTGTCGCTAGCAAA
P:12_48.5      GTTAAGGATGCATTTATTCAGATTTCATTTGTTTGGGT-------------------...------------------TGCATTTGCTCAGGATGCATTTGTTTAGCAGGTCCCTGTCGCTAGCAAA
H:M:3692       CCCCTTCGGCAAGGTCGAAGGGGGTTCGGTTGGTCTCTGCTAGTGTGGAGATAAATC...TTGTGATAAGGGTGGAGAGGTTAAAGGAGCCACTTATTAGTAATGTTGATAGTAGAATGATGGCTAG

H:13:109       CAGCTATTGCTGGCTAGCCTCCAAATTGGTCTCTAATTTGAGGTTGATCGGGGTTTATC...GAGTTTTTTACAACTCAGGTCTCTGTTGACTGTTGCAAAATGGTTCAGATACAAACTCTCTAACAC
P:13_110       CAGCTATTGCTGGCTAGCCTCCAAATTGGTCTCTAATTT--------------------...------------------GTCTCTGTTGACTGTTGCAAAATGGTTCAGATACAAACTCTCTAACAC
H:M:884        TGCTGAAGATGGCGGTATATAGGCTGAGCAAGAGGTGGTGAGGTTGATCGGGGTTTATC...GAGTTTTTTACAACTCAGGTGAGTTTTAGCTTTATTGGGGAGGGGGTGATCTAAAACACTCTTTAC
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H:13:55.4      AGTGGCTGCTCCATCTGCCTGGGTCTGAGAGTAAAGGGAATAGTAGGCCTCCTAGG...GAGTAATAGAAATGCGGTAATACAAAGCAGAATGCCCAGCCAGCTTGAAATTGACAGATGTTTATATAA
P:13_55.9      AGTGGCTGCTCCATCTGCCTGGGTCTGAGAGTAAA---------------------...---------------GGTAATACAAAGCAGAATGCCCAGCCAGCTTGAAATTGACAGATGTTTATATAA
H:M:5009       CTTCGATAATGGCCCATTTGGGCAAAAAGCCGGTTAGCGGGGGCAGGCCTCCTAGG...GAGTAGTAGGAATGCGGTAGTAGTTAGGATAATATAAATAGTTAAATTAAGAATGGTTATGTTAGGGTT

H:13:40.2      AAGCTGACGTGCTACAGCACTGCTTCTCAAACTTTAAGCTTAGCCCCCACCC...AATCCCCTGGAAGTCTTTAATATGCAT--AAAAATTTTTTTTTTTTGAGACAGGGCCTCACTCTGTCAGAC
P:13_52.1      AAGCTGATGTGCTACAGCACTGCTTCTCAAACTTTAA---------------...--------------------TATGCATAGAAATTATTTTTTTTTTTGAGACAGGGTCTCACTCTGTCACAC
H:M:9424       TTCTTCGCAGGATTTTTCTGAGCCTTTTACCACTCCAGCCTAGCCCCTACCC...AATCCCCTAGAAGTCCCACTCCTAAACACATCCGTATTACTCGCATCAGGAGTATCAATCACCTGAGCTCA

H:14:32.0      TGGTTTCCAGCATTATCCATGTCCCTGCAAGGGATAGGTGTTGGTATAGA...GGGTTTTGCAGTCCTTAGCTGCAAATGAGTCCTTAGCAAGGGACTCATTCTTTTTTATGGCTGCATAATATTCCAT
P:14_31.5      TGGTTTCCAGCATTATCCATGTCCCTGCAAGGGA---------------...-------------------------------------CATGAACTCATTCTTTTTTATGGCTGCATAATATTCCAT
H:M:5484       GAATATAAACTTCAGGGTGACCGAAAAATCAGAATAGGTGTTGGTATAGA...GGGTTTTGCAGTCCTTAGCTGTTGCAGAAATTAAGTATTGCAACTTACTGAGGGCTTTGAAGGCTCTTGGTCTGTA

H:17:48.5      TAAGAAGGATAGTAATTCTCTCATTGAGCTGCTGGGACACCTCCGCTACCA...GAAGGAATCGAACCCCCTGGGAGTATTACCTAAATGAATGCTTATGAAAGATTCCAGCACAATAGCTGAGTGCA
P:17_52.2      TAAGGAGGATAATAATTCTCTCGTTGAGCTGCTGGGA--------------...----------------------GTATTACCTAAATGAATGCTTATGAAAGATTCTAGCACAATAGCTGAGTGCA
H:M:6719       TTACAGTAGGAATAGACGTAGACACACGAGCATATTTCACCTCCGCTACCA...GAAGGAATCGAACCCCCCAAAGCTGGTTTCAAGCCAACCCCATGGCCTCCATGACTTTTTCAAAAAGGTATTAG

H:17:76.2      TTATGCTGTTGAATGACTTGGAATTAATTTGTAAGTGTAGAGAAAAATGAATCCTAGGGCTCAGAGCACTGCAGCAGATCACGTATTTTTGCTCTGTGACAAAGTATTTTTATTTTCACTTTTTC
P:17_80.8      TTATGCTGTTGAATGACTTGGAATTAATTTGTAAGTGTA----------------------------------TATATCCTCGTATTTTTGCTCCGTGACAAAGTATTTTTATTTTAACTTTTTC
H:M:6804       GTTTGCTAATACAATGCCAGTCAGGCCACCTACGGTGAAAAGAAAGATGAATCCTAGGGCTCAGAGCACTGCAGCAGATCATTTCATATTGCTTCCGTGGAGTGTGGCGAGTCAGCTAAATACTT

H:17:39.4      GAGAATAGACTCTAGTGGGCAAAAATGGAAGCAAGAAGGCTACATAGAAAAAT...CGCGTTCCTTTAAGGCCATTTAGGAAGCTATTTCTTCAACTCAGGGTGGTATCCTGGAGGAGGTGGGAA
P:17_13.6      GAGAATAGACTCTAGTGGGCAAAAATGGAAGCAAGAAGGC-------------...----------------CATTTAGGAAGCTATTTCTTCAACTCAGGGTGGTATCCTGGAGGAGGTGGGAA
H:M:10044      ACTAATAATTATTACATTTTGACTACCACAACTCAACGGCTACATAGAAAAAT...CGCGTCCCTTTCTC--CATAAAATTCTTCTTAGTAGCTATTACCTTCTTATTATTTGATCTAGAAATTG

H:18:43.6      CTGTAATCCCAGCTACTCGGAAGGCTAAGGCAGAAGAATGGCCGTAGTATACC...AAGGAGTCGCAGGTCGCCTCGCTTGAATCCAGGAGGCGGAGGTTGCAGTGAGCTGAGGGCATCCCACTG
P:18_44.0      CTGTAATCCCAGCTACTCGGAAGGCTAAGGCAGAAGAAT--------------...--------------------CGCTTGAATCCAGGAGGCGGAGGTTGCAGTGAGCTGAGGGCATCCCACTG
H:M:7876       GCATGAAACTGTGGTTTGCTCCACAGATTTCAGAGCATTGACCGTAGTATACC...AAGGAGTCGCAGGTCGCCTGGTTCTAGGAATAATGGGGGAAGTATGTAGGAGTTGAAGATTAGTCCGCC

H:18:28.3      ATTTTGAAGTCTGGAGACTCACTGAATTTGTTCTGGGTATGGGGGAGGTTACATG...GTGGGGTTAGCGATTCTGGTACAGTGGCTTGTGCCTGTAATCCCAGCACTTGGGAGGCCGAAGCAGGT
P:18.13.9      ATTTTGAAGTCTGGAGACTCACTGAATTTGTTCTGGGT-----------------...---------------CTGGTACAGTGGCTTGTGCCTGTAATTCCAGCACTTGGGAGGCCAAAGCAGGT
H:M:14282      TGTTAGCGGTGTGGTCGGGTGTGTTATTATTCTGAATTTTGGGGGAGGTTATATG...GTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAAGAGTATGATGGGGTGGTGGTTGTGGT

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H:18:28.3      ATTTTGAAGTCTGGAGACTCACTGAATTTGTTCTG-GGTATGGGGGAGGTTACATG...GTGGGGTTAGCGATTCTGGTACAG-TGG-CTTGTGCCTGTAATCCCAGCACTTGGGAGGCCGAAGCAGGT
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P:18.13.9      ATTTTGAAGTCTGGAGACTCACTGAATTTGTTCTG-GGT-----------------...---------------CTGGTACAG-TGG-CTTGTGCCTGTAATTCCAGCACTTGGGAGGCCAAAGCAGGT
H:M:14282      TGTTAGCGGTGTGGTCGGGTGTGTTATT-ATTCTGAATTTTGGGGGAGGTTATATG...GTGGGGTTAGCGATGGAGGTAGGATTGGTGCTGTGGGTGAAA--GAGTATGATGGGGTGGTGGTTGTGGT
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H:20:9.1       TCATCCTTGGCAGCCCCAACTCCTGCCTGTCAGCCCAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACCTTTCAAGCTCAAGTCTCCCTTTGCGGTTGCTACAACCACCAAGGGCTCATCCTC
P:20_9.1       TCATCCTTGGCAGCCCCAACTCCTGCCTGTCAGCCCAAG-------------------------------------------------------TCTCCCTTTGCGGTTGCTACAGCCACCAAGGGCTCATCCTC
H:M:2082       AGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCCTCACACCCAATTGGACCAATC


H:20:13.1      AAAATTATTTGATTATTGAGTCTTGATAATTATATCATCAACCATTACCCTCTACATCACCGCCCCGACCTTAGCTCTAATTATATCAGAGCCAAAAATGTGTCTTTGGTTAGATCTGTTGGAAAAGAG
P:20_13.2      AAAATTATTTGATTATTGAGTCTTGATAATTATATCA---------------------------------------------------GAGCCAAAAATGTGTCTTTGGTTAGATCTGTTGGAAAAGAG
H:M:3401       AAAACTCTTCACCAAAGAGCCCCTAAAACCCGCCACATCTACCATCACCCTCTACATCACCGCCCCGACCTTAGCTCTCACCATCGCTCTTCTACTATGAACCCCCCTCCCCATACCCAACCCCCTGGT


H:20:55.1      TTCAAATTCTAGCTTAACAGTGAATAAGTTTTAGTATAAGTATACCGCCTCACCCCAC...GGCCTTCACCCCTGCCCCCAAAACTGCATGGGACGTATGCCAAAAAGTATTTGTTATTTATCTG
P:20_54.7      TTCAAATTCTAGCTTAACAGTGAATAATTTTTAGTATAAGTATACC------------...---------------CCCCAAAACTGCATGGGACGTATGCCAAAAAGTACTTGTTATTTATCTG
H:M:12863      AACTCATGAGACCCACAACAAATAGCCCTTCTAAACGCTAATCCAAGCCTCACCCCAC...GGTCTCCACCCCTGACTCCCCTCAGCCATAGAAGGCCCCACCCCAGTCTCAGCCCTACTCCACT


H:22:34.6      TTTTAGGGAATGAAAGCTAGGTCGTTTCCCCGCATAAACAACATAAGCTTCTGACTCTTACCTCCCTCTTGATTTATTTAACCTCTGAATAGAT----GGTCTATATTTA
P:22_34.8      TTTTAGGGAATGAAAGCTAGG-------------------------------------------TCTTGATTTATTTAACCTCTGAATGAATAGATGGTCTATATTTA
H:M:6082       ATAATCGGTGCCCCCGATATGGCGTTTCCCCGCATAAACAACATAAGCTTCTGACTCTTACCTCCCTCTCTCCTACTCCTGCTCGCATCTGCTATAGTGGAGGCCGGAGC
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Yellow highlighted nucleotides represent BLAST-defined homology between human mtDNA and the human numt region. Boxed nucleotides are the actual nucleotides inserted, as inferred from comparison to chimp sequence, the proxy for the pre-integration target site. Italicized nucleotides indicate insertions in human, or deletions in chimp. Sequences are labeled by species (H=Homo, P=Pan), followed by chromosome number (or “M” for the mitochondrial genome), followed by beginning position rounded to the nearest Mb for nuclear DNA or nearest bp for mitochondrial DNA.